SEQUENCE LISTING

<110>   Bachmann, Martin F
        Maurer, Patrik F

<120>   Hapten-Carrier Conjugates and Uses Thereof

<130>   1700.0300001

<150>   US 60/396,575
<151>   2002-07-18

<160>   33

<170>   PatentIn version 3.2

<210>   1
<211>   185
<212>   PRT
<213>   Hepatitis B virus

<400>   1

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Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1               5                   10                  15


Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20                  25                  30


Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
        35                  40                  45


Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50                  55                  60


Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
65                  70                  75                  80


Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
            85                  90                  95


Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
            100                 105                 110


Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
            115                 120                 125


Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130                 135                 140


Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg
145                 150                 155                 160
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Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
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Arg Ser Gln Ser Arg Glu Ser Gln Cys
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<210> 2
<211> 182
<212> PRT
<213> Escherichia coli

<400> 2

Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
1   5   10   15

Ser Ser Thr Thr Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr
            20   25   30

Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
            35   40   45

Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
        50   55   60

Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
65   70   75   80

Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
            85   90   95

Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
            100   105   110

Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
        115   120   125

Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
    130   135   140

Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
145   150   155   160

Phe Ala Thr Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr
            165   170   175

Phe Lys Val Gln Tyr Gln
            180

<210> 3
<211> 132
<212> PRT
<213> Bacteriophage Qbeta

<400> 3

Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly Lys
1   5   10   15

Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
            20   25   30

Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
            35   40   45

Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
        50   55   60

Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
65   70   75   80

Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser Phe
            85   90   95

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
            100   105   110

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
            115   120   125

Asn Pro Ala Tyr
    130

<210> 4
<211> 329
<212> PRT
<213> Bacteriophage Qbeta

<400> 4

Met Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly
1   5   10   15

Lys Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
            20   25   30

```
Val Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
        35              40              45

Val Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
        50              55              60

Val Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser
65              70              75              80

Cys Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser
            85              90              95

Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu
            100             105             110

Leu Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln
        115             120             125

Leu Asn Pro Ala Tyr Trp Thr Leu Leu Ile Ala Gly Gly Gly Ser Gly
    130             135             140

Ser Lys Pro Asp Pro Val Ile Pro Asp Pro Pro Ile Asp Pro Pro Pro
145             150             155             160

Gly Thr Gly Lys Tyr Thr Cys Pro Phe Ala Ile Trp Ser Leu Glu Glu
            165             170             175

Val Tyr Glu Pro Pro Thr Lys Asn Arg Pro Trp Pro Ile Tyr Asn Ala
        180             185             190

Val Glu Leu Gln Pro Arg Glu Phe Asp Val Ala Leu Lys Asp Leu Leu
        195             200             205

Gly Asn Thr Lys Trp Arg Asp Trp Asp Ser Arg Leu Ser Tyr Thr Thr
    210             215             220

Phe Arg Gly Cys Arg Gly Asn Gly Tyr Ile Asp Leu Asp Ala Thr Tyr
225             230             235             240

Leu Ala Thr Asp Gln Ala Met Arg Asp Gln Lys Tyr Asp Ile Arg Glu
            245             250             255

Gly Lys Lys Pro Gly Ala Phe Gly Asn Ile Glu Arg Phe Ile Tyr Leu
            260             265             270
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Lys Ser Ile Asn Ala Tyr Cys Ser Leu Ser Asp Ile Ala Ala Tyr His
        275                 280                 285


Ala Asp Gly Val Ile Val Gly Phe Trp Arg Asp Pro Ser Ser Gly Gly
        290                 295                 300


Ala Ile Pro Phe Asp Phe Thr Lys Phe Asp Lys Thr Lys Cys Pro Ile
305             310                 315                 320


Gln Ala Val Ile Val Val Pro Arg Ala
                325
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<210>  5
<211>  28
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  p1.44 primer


<220>
<221>  misc_feature
<222>  (1)..(2)
<223>  n can be any nucleotide, preferably a

<400>  5
nnccatggca aataagccaa tgcaaccg                                          28


<210>  6
<211>  132
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Bacteriophage Qbeta 240 mutant

<400>  6
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Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Arg Asp Gly Lys
1               5                   10                  15


Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
            20                  25                  30


Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
        35                  40                  45


Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
    50                  55                  60


Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
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65   70   75   80

Asp Pro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe
                85   90   95

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
                100   105   110

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
                115   120   125

Asn Pro Ala Tyr
        130

<210> 7
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Bacteriophage Q-beta 243 mutant

<400> 7

Ala Lys Leu Glu Thr Val Thr Leu Gly Lys Ile Gly Lys Asp Gly Lys
1   5   10   15

Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
                20   25   30

Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
                35   40   45

Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
        50   55   60

Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
65   70   75   80

Asp Pro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe
                85   90   95

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
                100   105   110

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
                115   120   125

Asn Pro Ala Tyr
       130

<210> 8
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Bacteriophage Q-beta 250 mutant

<400> 8

Ala Arg Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Arg Asp Gly Lys
1   5   10   15

Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
            20   25   30

Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
        35   40   45

Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
    50   55   60

Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
65   70   75   80

Asp Pro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe
                85   90   95

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
            100   105   110

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
        115   120   125

Asn Pro Ala Tyr
       130

<210> 9
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Bacteriophage Q-beta 251 mutant

<400> 9

Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly Arg

```
1                    5                         10                        15
```

Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
            20   25   30

Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
            35   40   45

Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
        50   55   60

Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
65   70   75   80

Asp Pro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe
                85   90   95

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
            100   105   110

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
            115   120   125

Asn Pro Ala Tyr
        130

<210> 10
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Bacteriophage Q-beta 259 mutant

<400> 10

Ala Arg Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly Arg
1   5   10   15

Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
            20   25   30

Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
            35   40   45

Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
        50   55   60
```

Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
65                  70              75                  80

Asp Pro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe
            85                  90              95

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
            100             105             110

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
        115             120             125

Asn Pro Ala Tyr
    130


<210>  11
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  linker

<400>  11

Gly Gly Lys Gly Gly
1               5


<210>  12
<211>  49
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  GCN4

<400>  12

Pro Ala Ala Leu Lys Arg Ala Arg Asn Glu Ala Ala Arg Arg Ser Arg
1               5                   10              15

Ala Arg Lys Leu Gln Arg Met Lys Gln Leu Glu Asp Lys Val Glu Glu
            20                  25              30

Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala Arg Leu Lys
            35                  40              45

Lys


<210>  13

<211> 128
<212> PRT
<213> Bacteriophage PP7

<400> 13

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Met Ser Lys Thr Ile Val Leu Ser Val Gly Glu Ala Thr Arg Thr Leu
1               5                   10                  15

Thr Glu Ile Gln Ser Thr Ala Asp Arg Gln Ile Phe Glu Glu Lys Val
            20                  25                  30

Gly Pro Leu Val Gly Arg Leu Arg Leu Thr Ala Ser Leu Arg Gln Asn
        35                  40                  45

Gly Ala Lys Thr Ala Tyr Arg Val Asn Leu Lys Leu Asp Gln Ala Asp
    50                  55                  60

Val Val Asp Cys Ser Thr Ser Val Cys Gly Glu Leu Pro Lys Val Arg
65                  70                  75                  80

Tyr Thr Gln Val Trp Ser His Asp Val Thr Ile Val Ala Asn Ser Thr
                85                  90                  95

Glu Ala Ser Arg Lys Ser Leu Tyr Asp Leu Thr Lys Ser Leu Val Ala
            100                 105                 110

Thr Ser Gln Val Glu Asp Leu Val Val Asn Leu Val Pro Leu Gly Arg
            115                 120                 125
```

<210> 14
<211> 131
<212> PRT
<213> Bacteriophage AP205

<400> 14

```
Met Ala Asn Lys Pro Met Gln Pro Ile Thr Ser Thr Ala Asn Lys Ile
1               5                   10                  15

Val Trp Ser Asp Pro Thr Arg Leu Ser Thr Thr Phe Ser Ala Ser Leu
            20                  25                  30

Leu Arg Gln Arg Val Lys Val Gly Ile Ala Glu Leu Asn Asn Val Ser
        35                  40                  45

Gly Gln Tyr Val Ser Val Tyr Lys Arg Pro Ala Pro Lys Pro Glu Gly
    50                  55                  60
```

Cys Ala Asp Ala Cys Val Ile Met Pro Asn Glu Asn Gln Ser Ile Arg
65   70   75   80

Thr Val Ile Ser Gly Ser Ala Glu Asn Leu Ala Thr Leu Lys Ala Glu
              85   90   95

Trp Glu Thr His Lys Arg Asn Val Asp Thr Leu Phe Ala Ser Gly Asn
          100   105   110

Ala Gly Leu Gly Phe Leu Asp Pro Thr Ala Ala Ile Val Ser Ser Asp
        115   120   125

Thr Thr Ala
    130

<210> 15
<211> 3635
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid, pAP283-58, encoding RNA phage AP205 coat protein

<400> 15
cgagctcgcc cctggcttat cgaaattaat acgactcact ataggggagac cggaattcga   60

gctcgcccgg ggatcctcta gaattttctg cgcacccatc ccgggtggcg cccaaagtga   120

ggaaaatcac atggcaaata agccaatgca accgatcaca tctacagcaa ataaaattgt   180

gtggtcggat ccaactcgtt tatcaactac attttcagca agtctgttac gccaacgtgt   240

taaagttggt atagccgaac tgaataatgt ttcaggtcaa tatgtatctg tttataagcg   300

tcctgcacct aaaccggaag gttgtgcaga tgcctgtgtc attatgccga tgaaaacca   360

atccattcgc acagtgattt cagggtcagc cgaaaacttg ctaccttaa aagcagaatg   420

ggaaactcac aaacgtaacg ttgacacact cttcgcgagc ggcaacgccg gtttgggttt   480

ccttgaccct actgcggcta tcgtatcgtc tgatactact gcttaagctt gtattctata   540

gtgtcaccta atcgtatgt gtatgataca taaggttatg tattaattgt agccgcgttc   600

taacgacaat atgtacaagc ctaattgtgt agcatctggc ttactgaagc agaccctatc   660

atctctctcg taaactgccg tcagagtcgg tttggttgga cgaaccttct gagtttctgg   720

taacgccgtt ccgcaccccg gaaatggtca ccgaaccaat cagcagggtc atcgctagcc   780

agatcctcta cgccggacgc atcgtggccg gcatcaccgg cgccacaggt gcggttgctg   840

gcgcctatat cgccgacatc accgatgggg aagatcgggc tcgccacttc gggctcatga   900

gcgcttgttt cggcgtgggt atggtggcag ccccgtggc cgggggactg ttgggcgcca   960

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tctccttgca tgcaccattc cttgcggcgg cggtgctcaa cggcctcaac ctactactgg    1020

gctgcttcct aatgcaggag tcgcataagg gagagcgtcg atatggtgca ctctcagtac    1080

aatctgctct gatgccgcat agttaagcca actccgctat cgctacgtga ctgggtcatg    1140

gctgcgcccc gacacccgcc aacacccgct gacgcgccct gacgggcttg tctgctcccg    1200

gcatccgctt acagacaagc tgtgaccgtc tccgggagct gcatgtgtca gaggttttca    1260

ccgtcatcac cgaaacgcgc gaggcagctt gaagacgaaa gggcctcgtg atacgcctat    1320

ttttataggt taatgtcatg ataataatgg tttcttagac gtcaggtggc acttttcggg    1380

gaaatgtgcg cggaacccct atttgtttat ttttctaaat acattcaaat atgtatccgc    1440

tcatgagaca ataaccctga taaatgcttc aataatattg aaaaaggaag agtatgagta    1500

ttcaacattt ccgtgtcgcc cttattccct tttttgcggc attttgcctt cctgtttttg    1560

ctcacccaga aacgctggtg aaagtaaaag atgctgaaga tcagttgggt gcacgagtgg    1620

gttacatcga actggatctc aacagcggta agatccttga gagttttcgc cccgaagaac    1680

gttttccaat gatgagcact tttaaagttc tgctatgtgg cgcggtatta tcccgtattg    1740

acgccgggca agagcaactc ggtcgccgca tacactattc tcagaatgac ttggttgagt    1800

actcaccagt cacagaaaag catcttacgg atggcatgac agtaagagaa ttatgcagtg    1860

ctgccataac catgagtgat aacactgcgg ccaacttact tctgacaacg atcggaggac    1920

cgaaggagct aaccgctttt ttgcacaaca tgggggatca tgtaactcgc cttgatcgtt    1980

gggaaccgga gctgaatgaa gccataccaa acgacgagcg tgacaccacg atgcctgtag    2040

caatggcaac aacgttgcgc aaactattaa ctggcgaact acttactcta gcttcccggc    2100

aacaattaat agactggatg gaggcggata aagttgcagg accacttctg cgctcggccc    2160

ttccggctgg ctggtttatt gctgataaat ctggagccgg tgagcgtggg tctcgcggta    2220

tcattgcagc actggggcca gatggtaagc cctcccgtat cgtagttatc tacacgacgg    2280

ggagtcaggc aactatggat gaacgaaata gacagatcgc tgagataggt gcctcactga    2340

ttaagcattg gtaactgtca gaccaagttt actcatatat actttagatt gatttaaaac    2400

ttcattttta atttaaaagg atctaggtga agatcctttt tgataatctc atgaccaaaa    2460

tcccttaacg tgagttttcg ttccactgag cgtcagaccc cgtagaaaag atcaaaggat    2520

cttcttgaga tccttttttt ctgcgcgtaa tctgctgctt gcaaacaaaa aaaccaccgc    2580

taccagcggt ggtttgtttg ccggatcaag agctaccaac tctttttccg aaggtaactg    2640

gcttcagcag agcgcagata ccaaatactg tccttctagt gtagccgtag ttaggccacc    2700

acttcaagaa ctctgtagca ccgcctacat acctcgctct gctaatcctg ttaccagtgg    2760

ctgctgccag tggcgataag tcgtgtctta ccgggttgga ctcaagacga tagttaccgg    2820
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ataaggcgca gcggtcgggc tgaacggggg gttcgtgcac acagcccagc ttggagcgaa      2880

cgacctacac cgaactgaga tacctacagc gcgagcattg agaaagcgcc acgcttcccg      2940

aagggagaaa ggcggacagg tatccggtaa gcggcagggt cggaacagga gagcgcacga      3000

gggagcttcc aggggggaaac gcctggtatc tttatagtcc tgtcgggttt cgccacctct     3060

gacttgagcg tcgatttttg tgatgctcgt caggggggcg gagcctatgg aaaaacgcca      3120

gcaacgcggc ctttttacgg ttcctggcct tttgctggcc ttttgctcac atgttctttc      3180

ctgcgttatc ccctgattct gtggataacc gtattaccgc ctttgagtga gctgataccg      3240

ctcgccgcag ccgaacgacc gagcgcagcg agtcagtgag cgaggaagcg aagagcgcc       3300

caatacgcaa accgcctctc cccgcgcgtt ggccgattca ttaatgcagc tgtggtgtca      3360

tggtcggtga tcgccagggt gccgacgcgc atctcgactg catggtgcac caatgcttct      3420

ggcgtcaggc agccatcgga agctgtggta tggccgtgca ggtcgtaaat cactgcataa      3480

ttcgtgtcgc tcaaggcgca ctcccgttct ggataatgtt ttttgcgccg acatcataac      3540

ggttctggca aatattctga aatgagctgt tgacaattaa tcatcgaact agttaactag      3600

tacgcaagtt cacgtaaaaa gggtatcgcg gaatt                                 3635
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<210> 16
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> putative AP205 ribosomal binding site of plasmid pAP283-58

<400> 16
tctagaattt tctgcgcacc catcccgggt ggcgcccaaa gtgaggaaaa tcacatg   57

<210> 17
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Shine Delagarno sequence of vector pQb185

<400> 17
tctagattaa cccaacgcgt aggagtcagg ccatg   35

<210> 18
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Bacteriophage AP205 mutant

<400> 18

Met Ala Asn Lys Thr Met Gln Pro Ile Thr Ser Thr Ala Asn Lys Ile
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Val Trp Ser Asp Pro Thr Arg Leu Ser Thr Thr Phe Ser Ala Ser Leu
            20   25   30

Leu Arg Gln Arg Val Lys Val Gly Ile Ala Glu Leu Asn Asn Val Ser
        35   40   45

Gly Gln Tyr Val Ser Val Tyr Lys Arg Pro Ala Pro Lys Pro Glu Gly
    50   55   60

Cys Ala Asp Ala Cys Val Ile Met Pro Asn Glu Asn Gln Ser Ile Arg
65   70   75   80

Thr Val Ile Ser Gly Ser Ala Glu Asn Leu Ala Thr Leu Lys Ala Glu
            85   90   95

Trp Glu Thr His Lys Arg Asn Val Asp Thr Leu Phe Ala Ser Gly Asn
            100   105   110

Ala Gly Leu Gly Phe Leu Asp Pro Thr Ala Ala Ile Val Ser Ser Asp
        115   120   125

Thr Thr Ala
    130

<210> 19
<211> 3613
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid, pAP281-32, encoding RNA phage AP205 coat protein

<400> 19
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gctcgcccgg ggatcctcta gattaaccca acgcgtagga gtcaggccat ggcaaataag   120

acaatgcaac cgatcacatc tacagcaaat aaaattgtgt ggtcggatcc aactcgttta   180

tcaactacat tttcagcaag tctgttacgc caacgtgtta agttggtat agccgaactg   240

aataatgttt caggtcaata tgtatctgtt ataagcgtc ctgcacctaa accggaaggt   300

tgtgcagatg cctgtgtcat tatgccgaat gaaaaccaat ccattcgcac agtgatttca   360

gggtcagccg aaaacttggc taccttaaaa gcagaatggg aaactcacaa acgtaacgtt   420

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gacacactct tcgcgagcgg caacgccggt ttgggtttcc ttgaccctac tgcggctatc      480

gtatcgtctg atactactgc ttaagcttgt attctatagt gtcacctaaa tcgtatgtgt      540

atgatacata aggttatgta ttaattgtag ccgcgttcta acgacaatat gtacaagcct      600

aattgtgtag catctggctt actgaagcag accctatcat ctctctcgta aactgccgtc      660

agagtcggtt tggttggacg aaccttctga gtttctggta acgccgttcc gcaccccgga      720

aatggtcacc gaaccaatca gcagggtcat cgctagccag atcctctacg ccggacgcat      780

cgtggccggc atcaccggcg ccacaggtgc ggttgctggc gcctatatcg ccgacatcac      840

cgatggggaa gatcgggctc gccacttcgg gctcatgagc gcttgtttcg gcgtgggtat      900

ggtggcaggc cccgtggccg ggggactgtt gggcgccatc tccttgcatg caccattcct      960

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ggcagcttga agacgaaagg gcctcgtgat acgcctattt ttataggtta atgtcatgat     1320

aataatggtt tcttagacgt caggtggcac ttttcgggga aatgtgcgcg gaacccctat     1380

ttgtttattt ttctaaatac attcaaatat gtatccgctc atgagacaat aaccctgata     1440

aatgcttcaa taatattgaa aaaggaagag tatgagtatt caacatttcc gtgtcgccct     1500

tattcccttt tttgcggcat tttgccttcc tgtttttgct cacccagaaa cgctggtgaa     1560

agtaaaagat gctgaagatc agttgggtgc acgagtgggt tacatcgaac tggatctcaa     1620

cagcggtaag atccttgaga gttttcgccc cgaagaacgt tttccaatga tgagcacttt     1680

taaagttctg ctatgtggcg cggtattatc ccgtattgac gccgggcaag agcaactcgg     1740

tcgccgcata cactattctc agaatgactt ggttgagtac tcaccagtca cagaaaagca     1800

tcttacggat ggcatgacag taagagaatt atgcagtgct gccataacca tgagtgataa     1860

cactgcggcc aacttacttc tgacaacgat cggaggaccg aaggagctaa ccgctttttt     1920

gcacaacatg ggggatcatg taactcgcct tgatcgttgg gaaccggagc tgaatgaagc     1980

cataccaaac gacgagcgtg acaccacgat gcctgtagca atggcaacaa cgttgcgcaa     2040

actattaact ggcgaactac ttactctagc ttcccggcaa caattaatag actggatgga     2100

ggcggataaa gttgcaggac cacttctgcg ctcggccctt ccggctggct ggtttattgc     2160

tgataaatct ggagccggtg agcgtgggtc tcgcggtatc attgcagcac tggggccaga     2220
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tggtaagccc tcccgtatcg tagttatcta cacgacgggg agtcaggcaa ctatggatga    2280

acgaaataga cagatcgctg agataggtgc ctcactgatt aagcattggt aactgtcaga    2340

ccaagtttac tcatatatac tttagattga tttaaaactt catttttaat ttaaaaggat    2400

ctaggtgaag atcctttttg ataatctcat gaccaaaatc ccttaacgtg agttttcgtt    2460

ccactgagcg tcagaccccg tagaaaagat caaaggatct tcttgagatc cttttttct     2520

gcgcgtaatc tgctgcttgc aaacaaaaaa accaccgcta ccagcggtgg tttgtttgcc    2580

ggatcaagag ctaccaactc tttttccgaa ggtaactggc ttcagcagag cgcagatacc    2640

aaatactgtc cttctagtgt agccgtagtt aggccaccac ttcaagaact ctgtagcacc    2700

gcctacatac ctcgctctgc taatcctgtt accagtggct gctgccagtg gcgataagtc    2760

gtgtcttacc gggttggact caagacgata gttaccggat aaggcgcagc ggtcgggctg    2820

aacggggggt tcgtgcacac agcccagctt ggagcgaacg acctacaccg aactgagata    2880

cctacagcgc gagcattgag aaagcgccac gcttcccgaa gggagaaagg cggacaggta    2940

tccggtaagc ggcagggtcg aacaggaga gcgcacgagg gagcttccag ggggaaacgc      3000

ctggtatctt tatagtcctg tcgggtttcg ccacctctga cttgagcgtc gattttgtg     3060

atgctcgtca ggggggcgga gcctatggaa aaacgccagc aacgcggcct ttttacggtt    3120

cctggccttt tgctggcctt ttgctcacat gttctttcct gcgttatccc ctgattctgt    3180

ggataaccgt attaccgcct ttgagtgagc tgataccgct cgccgcagcc gaacgaccga    3240

gcgcagcgag tcagtgagcg aggaagcgga agagcgccca atacgcaaac cgcctctccc    3300

cgcgcgttgg ccgattcatt aatgcagctg tggtgtcatg gtcggtgatc gccagggtgc    3360

cgacgcgcat ctcgactgca tggtgcacca atgcttctgg cgtcaggcag ccatcggaag    3420

ctgtggtatg gccgtgcagg tcgtaaatca ctgcataatt cgtgtcgctc aaggcgcact    3480

cccgttctgg ataatgtttt ttgcgccgac atcataacgg ttctggcaaa tattctgaaa    3540

tgagctgttg acaattaatc atcgaactag ttaactagta cgcaagttca cgtaaaaagg    3600

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<210>   20
<211>   30
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   p1.45 primer

<220>
<221>   misc_feature
<222>   (1)..(2)

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<223>  n can be any nucleotide,  preferably a

<400>  20
nntctagaat tttctgcgca cccatcccgg                                    30


<210>  21
<211>  31
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  p1.46 primer


<220>
<221>  misc_feature
<222>  (1)..(2)
<223>  n can be any nucleotide, preferably a

<400>  21
nnaagcttaa gcagtagtat cagacgatac g                                  31


<210>  22
<211>  43
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  p1.47 primer

<400>  22
gagtgatcca actcgtttat caactacatt ttcagcaagt ctg                     43


<210>  23
<211>  43
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  p1.48 primer

<400>  23
cagacttgct gaaaatgtag ttgataaacg agttggatca ctc                     43


<210>  24
<211>  129
<212>  PRT
<213>   Bacteriophage R17

<400>  24

Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asn Asp Gly Gly Thr Gly
1               5                   10                  15


Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp
            20                  25                  30
```

Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
    35   40   45

Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
    50   55   60

Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala
65   70   75   80

Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala
          85   90   95

Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu
        100   105   110

Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
      115   120   125

Tyr

<210>   25
<211>   130
<212>   PRT
<213>   Bacteriophage fr

<400>   25

Met Ala Ser Asn Phe Glu Glu Phe Val Leu Val Asp Asn Gly Gly Thr
1   5   10   15

Gly Asp Val Lys Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
        20   25   30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
      35   40   45

Val Arg Gln Ser Ser Ala Asn Asn Arg Lys Tyr Thr Val Lys Val Glu
    50   55   60

Val Pro Lys Val Ala Thr Gln Val Gln Gly Gly Val Glu Leu Pro Val
65   70   75   80

Ala Ala Trp Arg Ser Tyr Met Asn Met Glu Leu Thr Ile Pro Val Phe
          85   90   95

Ala Thr Asn Asp Asp Cys Ala Leu Ile Val Lys Ala Leu Gln Gly Thr
        100   105   110

Phe Lys Thr Gly Asn Pro Ile Ala Thr Ala Ile Ala Ala Asn Ser Gly
        115   120   125

Ile Tyr
    130

<210>   26
<211>   130
<212>   PRT
<213>   Bacteriophage GA

<400>   26

Met Ala Thr Leu Arg Ser Phe Val Leu Val Asp Asn Gly Gly Thr Gly
1   5   10   15

Asn Val Thr Val Val Pro Val Ser Asn Ala Asn Gly Val Ala Glu Trp
            20   25   30

Leu Ser Asn Asn Ser Arg Ser Gln Ala Tyr Arg Val Thr Ala Ser Tyr
        35   40   45

Arg Ala Ser Gly Ala Asp Lys Arg Lys Tyr Ala Ile Lys Leu Glu Val
    50   55   60

Pro Lys Ile Val Thr Gln Val Val Asn Gly Val Glu Leu Pro Gly Ser
65   70   75   80

Ala Trp Lys Ala Tyr Ala Ser Ile Asp Leu Thr Ile Pro Ile Phe Ala
            85   90   95

Ala Thr Asp Asp Val Thr Val Ile Ser Lys Ser Leu Ala Gly Leu Phe
        100   105   110

Lys Val Gly Asn Pro Ile Ala Glu Ala Ile Ser Ser Gln Ser Gly Phe
        115   120   125

Tyr Ala
    130

<210>   27
<211>   132
<212>   PRT
<213>   Bacteriophage SP

<400>   27

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Met Ala Lys Leu Asn Gln Val Thr Leu Ser Lys Ile Gly Lys Asn Gly
1               5                   10                  15

Asp Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly
            20              25                  30

Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
        35              40                  45

Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Phe Lys
    50              55                  60

Val Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Arg Asp Ala Cys
65                  70              75                  80

Asp Pro Ser Val Thr Arg Ser Ala Phe Ala Asp Val Thr Leu Ser Phe
            85              90                  95

Thr Ser Tyr Ser Thr Asp Glu Glu Arg Ala Leu Ile Arg Thr Glu Leu
            100             105                 110

Ala Ala Leu Leu Ala Asp Pro Leu Ile Val Asp Ala Ile Asp Asn Leu
        115             120                 125

Asn Pro Ala Tyr
        130
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<210> 28
<211> 329
<212> PRT
<213> Bacteriophage SP

<400> 28

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Ala Lys Leu Asn Gln Val Thr Leu Ser Lys Ile Gly Lys Asn Gly Asp
1               5                   10                  15

Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly Val
            20              25                  30

Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
        35              40                  45

Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Phe Lys Val
    50              55                  60

Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Arg Asp Ala Cys Asp
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<pre>
65   70   75   80

Pro Ser Val Thr Arg Ser Ala Phe Ala Asp Val Thr Leu Ser Phe Thr
                85   90   95

Ser Tyr Ser Thr Asp Glu Glu Arg Ala Leu Ile Arg Thr Glu Leu Ala
            100   105   110

Ala Leu Leu Ala Asp Pro Leu Ile Val Asp Ala Ile Asp Asn Leu Asn
        115   120   125

Pro Ala Tyr Trp Ala Ala Leu Leu Val Ala Ser Ser Gly Gly Gly Asp
    130   135   140

Asn Pro Ser Asp Pro Asp Val Pro Val Val Pro Asp Val Lys Pro Pro
145   150   155   160

Asp Gly Thr Gly Arg Tyr Lys Cys Pro Phe Ala Cys Tyr Arg Leu Gly
            165   170   175

Ser Ile Tyr Glu Val Gly Lys Glu Gly Ser Pro Asp Ile Tyr Glu Arg
            180   185   190

Gly Asp Glu Val Ser Val Thr Phe Asp Tyr Ala Leu Glu Asp Phe Leu
        195   200   205

Gly Asn Thr Asn Trp Arg Asn Trp Asp Gln Arg Leu Ser Asp Tyr Asp
    210   215   220

Ile Ala Asn Arg Arg Arg Cys Arg Gly Asn Gly Tyr Ile Asp Leu Asp
225   230   235   240

Ala Thr Ala Met Gln Ser Asp Asp Phe Val Leu Ser Gly Arg Tyr Gly
            245   250   255

Val Arg Lys Val Lys Phe Pro Gly Ala Phe Gly Ser Ile Lys Tyr Leu
            260   265   270

Leu Asn Ile Gln Gly Asp Ala Trp Leu Asp Leu Ser Glu Val Thr Ala
        275   280   285

Tyr Arg Ser Tyr Gly Met Val Ile Gly Phe Trp Thr Asp Ser Lys Ser
    290   295   300

Pro Gln Leu Pro Thr Asp Phe Thr Gln Phe Asn Ser Ala Asn Cys Pro
305   310   315   320
</pre>

Val Gln Thr Val Ile Ile Ile Pro Ser
                325

<210> 29
<211> 130
<212> PRT
<213> Bacteriophage MS2

<400> 29

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1   5   10   15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
            20   25   30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
            35   40   45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
    50   55   60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65   70   75   80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
            85   90   95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
            100   105   110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
            115   120   125

Ile Tyr   ,
    130

<210> 30
<211> 133
<212> PRT
<213> Bacteriophage M11

<400> 30

Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Lys Gly
1   5   10   15

Asp Val Thr Leu Asp Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly

```
                 20                        25                        30


     Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
             35                  40                  45


     Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
             50                  55                  60


     Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr
     65                  70                  75                  80


     Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ser Asp Val Thr Phe Ser
                     85                  90                  95


     Phe Thr Gln Tyr Ser Thr Val Glu Glu Arg Ala Leu Val Arg Thr Glu
                     100                 105                 110


     Leu Gln Ala Leu Leu Ala Asp Pro Met Leu Val Asn Ala Ile Asp Asn
             115                 120                 125


     Leu Asn Pro Ala Tyr
         130


     <210>   31
     <211>   133
     <212>   PRT
     <213>   Bacteriophage MX1

     <400>   31

     Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Asn Gly
     1                   5                   10                  15


     Asp Val Thr Leu Asn Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
                     20                  25                  30


     Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
             35                  40                  45


     Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
             50                  55                  60


     Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr
     65                  70                  75                  80


     Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ala Asp Val Thr Phe Ser
                     85                  90                  95
```

Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Leu Val Arg Thr Glu
            100   105   110

Leu Lys Ala Leu Leu Ala Asp Pro Met Leu Ile Asp Ala Ile Asp Asn
        115   120   125

Leu Asn Pro Ala Tyr
    130

<210> 32
<211> 330
<212> PRT
<213> Bacteriophage NL95

<400> 32

Met Ala Lys Leu Asn Lys Val Thr Leu Thr Gly Ile Gly Lys Ala Gly
1   5   10   15

Asn Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly
            20   25   30

Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
        35   40   45

Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
    50   55   60

Val Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Lys Asp Ala Cys
65   70   75   80

Asp Pro Ser Val Thr Arg Ser Gly Ser Arg Asp Val Thr Leu Ser Phe
            85   90   95

Thr Ser Tyr Ser Thr Glu Arg Glu Arg Ala Leu Ile Arg Thr Glu Leu
            100   105   110

Ala Ala Leu Leu Lys Asp Asp Leu Ile Val Asp Ala Ile Asp Asn Leu
        115   120   125

Asn Pro Ala Tyr Trp Ala Ala Leu Leu Ala Ala Ser Pro Gly Gly Gly
    130   135   140

Asn Asn Pro Tyr Pro Gly Val Pro Asp Ser Pro Asn Val Lys Pro Pro
145   150   155   160

Gly Gly Thr Gly Thr Tyr Arg Cys Pro Phe Ala Cys Tyr Arg Arg Gly

```
                165                      170                      175

     Glu Leu Ile Thr Glu Ala Lys Asp Gly Ala Cys Ala Leu Tyr Ala Cys
             180                 185                 190

     Gly Ser Glu Ala Leu Val Glu Phe Glu Tyr Ala Leu Glu Asp Phe Leu
             195                 200                 205

     Gly Asn Glu Phe Trp Arg Asn Trp Asp Gly Arg Leu Ser Lys Tyr Asp
         210                 215                 220

     Ile Glu Thr His Arg Arg Cys Arg Gly Asn Gly Tyr Val Asp Leu Asp
     225                 230                 235                 240

     Ala Ser Val Met Gln Ser Asp Glu Tyr Val Leu Ser Gly Ala Tyr Asp
                 245                 250                 255

     Val Val Lys Met Gln Pro Pro Gly Thr Phe Asp Ser Pro Arg Tyr Tyr
             260                 265                 270

     Leu His Leu Met Asp Gly Ile Tyr Val Asp Leu Ala Glu Val Thr Ala
             275                 280                 285

     Tyr Arg Ser Tyr Gly Met Val Ile Gly Phe Trp Thr Asp Ser Lys Ser
         290                 295                 300

     Pro Gln Leu Pro Thr Asp Phe Thr Arg Phe Asn Arg His Asn Cys Pro
     305                 310                 315                 320

     Val Gln Thr Val Ile Val Ile Pro Ser Leu
                 325                 330


<210>   33
<211>   129
<212>   PRT
<213>   Bacteriophage f2

<400>   33

Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asn Asp Gly Gly Thr Gly
1               5                   10                  15


Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp
            20                  25                  30


Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
        35                  40                  45
```

Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
    50   55   60

Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala
65   70   75   80

Ala Trp Arg Ser Tyr Leu Asn Leu Glu Leu Thr Ile Pro Ile Phe Ala
          85   90   95

Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu
        100   105   110

Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
        115   120   125

Tyr